Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

1-60 (cancelled)

61 (Previously presented). A method of using a model of a nuclear hormone receptor, or ligand binding domain thereof, bound to a nuclear hormone receptor ligand, the method comprising:

providing structural information corresponding to an atomic coordinate model of the nuclear hormone receptor, or ligand binding domain thereof, bound to the nuclear hormone receptor ligand; and,

accessing the structural information.

62 (Previously presented). A method of determining whether a potential nuclear ligand is likely to bind to a nuclear hormone receptor ligand binding domain, the method comprising:

accessing structural information corresponding to an atomic coordinate model of the nuclear hormone receptor ligand binding domain;

accessing structural information corresponding to the ligand; and,

modeling binding of the potential ligand to the nuclear hormone receptor ligand binding domain, thereby determining whether the potential ligand is likely to bind to the nuclear receptor ligand binding domain.

63 (Previously presented). The method of claim **62**, wherein modeling binding of the potential ligand comprises modeling whether the ligand binding domain folds around the potential ligand to form a buried ligand binding cavity.

64 (Previously presented). The method of claim **61** or **62**, wherein, in the atomic coordinate model, the nuclear receptor folds around the ligand or potential ligand to form a buried ligand binding cavity.

65 (Previously presented). The method of claim **61** or **62**, wherein the atomic coordinate model of the nuclear hormone receptor ligand binding domain comprises structural information for a bound ligand.

66 (Previously presented). The method of claim **61** or **62**, wherein the structural information comprises information corresponding to data from Appendix 3, 4, 5, 6, 7 or 8.

67 (Currently amended). The method of claim **61** or **62**, wherein accessing the structural information comprises performing a ~~Forrier~~Fourier transform of crystallographic data corresponding to the nuclear receptor, the nuclear receptor ligand binding domain, or the nuclear receptor bound to the ligand at the nuclear receptor ligand binding domain.

68 (Currently amended). The method of claim **61** or **62**, comprising modeling which amino acid or amino acids of the nuclear receptor or nuclear receptor ligand binding domain interact with at least a first chemical moiety of the ligand.

69 (Previously presented). The method of claim **68**, further comprising designing a modified ligand, which modified ligand is selected to increase or decrease a modeled interaction between the amino acid or amino acids and the first chemical moiety.

70 (Currently amended). The method of claim **61** or **62**, comprising crystallizing the nuclear hormone receptor bound to the nuclear receptor ligand, wherein the structural information is derived from a crystal structure of the resulting crystal.

71 (Previously presented). The method of claim **61** or **62**, wherein the ligand is a computationally designed ligand.

72 (Previously presented). The method of claim **61** or **62**, wherein the ligand is a compound of Formula 1.

73 (Previously presented). The method of claim **61** or **62**, wherein the nuclear hormone receptor is a TR receptor.

74 (Previously presented). The method of claim **61** or **62**, wherein the nuclear hormone receptor is selected from the group consisting of: a glucocorticoid receptor, an androgen receptor, a progestin receptor, an estrogen receptor, a vitamin D receptor, a retinoid receptor, an icosanoid receptor, and a peroxisome receptor.

75 (Currently amended). A method for identifying a compound capable of selectively modulating the activity of a thyroid hormone receptor (TR) isoform, said method comprising:

modeling test compounds that fit spatially and preferentially into a TR ligand binding domain (TR LBD) isoform of interest using an atomic structural model of a TR LBD isoform bound to a test compound, wherein said atomic structural model employs 2.0Å to 3.0Å~~high~~ resolution structural information corresponding to an atomic coordinate model of the thyroid hormone receptor, or ligand binding domain thereof, bound to the thyroid hormone receptor ligand,

screening said test compounds in a biological assay for TR isoform activity characterized by binding of a test compound to a TR LBD isoform, and

identifying a test compound that selectively modulates the activity of a TR isoform.

76 (Currently amended). The method of claim **75,** wherein said atomic structural model employs ~~high resolution~~ structural information corresponding to data from Appendix 3, 4, 5, 6, 7 or 8.

77 (Currently amended). A method for identifying a thyroid hormone receptor (TR) agonist or antagonist ligand, said method comprising the steps of:

providing the atomic coordinates of a TR ligand binding domain (TR LBD) to a computerized modeling system, wherein said atomic coordinates are based on 2.0Å to 3.0Å~~high~~ resolution structural information corresponding to an atomic coordinate model of the thyroid hormone receptor, or ligand binding domain thereof, bound to the thyroid hormone receptor ligand;

modeling ligands which fit spatially into the TR LBD; and

identifying in a biological assay for TR activity a ligand which increases or decreases the activity of said TR, whereby a TR agonist or antagonist is identified.

78 (Previously presented). The method of claim **77**, wherein said atomic coordinates are based on data from Appendix 3, 4, 5, 6, 7 or 8.

79 (Currently amended). A method of identifying a compound that selectively modulates an activity of a thyroid hormone receptor (TR) compared to other nuclear hormone receptors, said method comprising:

modeling compounds which fit spatially into a TR ligand binding domain (TR LBD) using an atomic structural model of a TR LBD, wherein said atomic structural model employs 2.0Å to 3.0Å~~high~~ resolution structural information corresponding to an atomic coordinate model of the thyroid hormone receptor, or ligand binding domain thereof, bound to the thyroid hormone receptor ligand;

selecting a compound comprising conformationally constrained structural features that interact with conformationally constrained residues of a TR LBD; and,

identifying in a biological assay for TR activity a compound that selectively binds to a TR LBD compared to other nuclear receptors, whereby a compound that selectively modulates a TR is identified.

80 (Currently amended). The method of claim **79**, wherein said atomic structural model employs ~~high resolution~~ structural information corresponding to data from Appendix 3, 4, 5, 6, 7 or 8.

81 (Currently amended). A method for identifying a thyroid hormone receptor (TR) agonist or antagonist ligand that selectively modulates an activity of a TR compared to other nuclear receptors, said method comprising the steps of:

providing the atomic coordinates of a TR ligand binding domain (TR LBD) to a computerized modeling system, wherein said atomic coordinates are based on 2.0Å to 3.0Å~~high~~ resolution structural information corresponding to an atomic coordinate model of the thyroid hormone receptor, or ligand binding domain thereof, bound to the thyroid hormone receptor ligand;

modeling ligands which fit spatially into the TR LBD and which interact with conformationally constrained residues of a TR LBD conserved among TR isoforms; and,

identifying in a biological assay for TR activity a ligand which selectively binds to said TR and increases or decreases the activity of said TR, whereby a TR agonist or antagonist that selectively modulates the activity of a TR is identified.

82 (Previously presented). The method of claim **81**, wherein said atomic coordinates are based on data from Appendix 3, 4, 5, 6, 7 or 8.